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SEQUENCE LISTING
  10> DYAX Corp.
      Ley, Arthur C.
      Luneau, Christopher J.
      Ladner, Robert C
<120> NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
<130> DYX-\(\frac{1}{2}.1\) US, DYX-012.1 PCT
<140> not yet assigned
<141>
       2001-06-19
<150> US 09/597,321
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DSHYS.JS1901
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<223> Xaa is any amino acid
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<211> 7
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<222> (7)..(7)
<223> Xaa is any amino acid
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<223> Xaal is an optional amino acid which, if present, is Ala, Asp, Gl
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<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa3 is an optional amino acid which, if present, is Asp, Glu, Ph
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DSEHTET .CELGOJ
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<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa4 is Ala, Asp, Glu, or Thr
<220>
<221> MISC_FEATURE
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Xaa Xaa Xaa Asp Arg Xaa
<210> 207
<211> 7
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<221> MISC_FEATURE
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<223> Xaal is an optional amino acid which, if present, is Asp or Glu
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<222> (2)..(2)
<223> Xaa2 is an optional amino acid which, if present, is Val
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<222> (3)..(3)
<223> Xaa3 is an optional amino acid which, if present, is Tyr
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<222> (4)..(4)
<223> Xaa4 is Asp, Glu or Ser
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<220>
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<223> Xaa7 is any amino acid
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Asp Ile Asn Asp Asp Arg
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Gly Asn Tyr Thr Asp Arg
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<211> 7
<212> PRT
<213> streptavidin binding sequence
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Trp His Pro Gln Phe Ser Ser
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<210> 211
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Pro Cys His Pro Gln Phe Pro Arg Cys Tyr 1 5 10

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<213> Bacteriophage M13mp18

<400> 212

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<212> PRT

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<400> 213

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Asn Ser Phe Thr Asn Val Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr 35 40 45

Ala Asn Tyr Glu Gly Cys Leu Trp Asn Ala Thr Gly Val Val Cys 50 55 60

Thr Gly Asp Glu Thr Gln Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu 65 70 75 80

Ala Ile Pro Glu Asn Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu 85 90 95

Gly Gly Gly Ser Glu Gly Gly Gly Thr Lys Pro Pro Glu Tyr Gly Asp

100 105 110

Thr Pro Ile Pro Gly Tyr Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr 115 120 125

Pro Pro Gly Thr Glu Gln Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu 130 135 140

Glu Ser Gln Pro Leu Asn Thr Phe Met Phe Gln Asn Asn Arg Phe Arg 145 150 155 160

Asn Arg Gln Gly Ala Leu Thr Val Tyr Thr Gly Thr Val Thr Gln Gly
165 170 175

Thr Asp Pro Val Lys Thr Tyr Tyr Gln Tyr Thr Pro Val Ser Ser Lys 180 185 190

Ala Met Tyr Asp Ala Tyr Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe 195 200 205

His Ser Gly Phe Asn Glu Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln 210 215 220

Ser Ser Asp Leu Pro Gln Pro Pro Val Asn Ala Gly Gly Gly Ser Gly 225 230 235 240

Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Gly Gly Gly Gly 245 250 255

Ser Glu Gly Gly Ser Glu Gly Gly Ser Gly Gly Gly Ser Gly 260 265 270

Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala 275 280 285

Met	Thr 290	Glu	Asn	Ala	Asp	Glu 295	Asn	Ala	Leu	GIn	300	Asp	Ala	гув	GIY	
Lys 305	Leu	Asp	Ser	Val	Ala 310	Thr	Asp	Tyr	Gly	Ala 315	Ala	Ile	Asp	Gly	Phe 320	
Ile	Gly	Asp	Val	Ser 325	Gly	Leu	Ala	Asn	Gly 330	Asn	Gly	Ala	Thr	Gly 335	Asp	
Phe	Ala	Gly	Ser 340	Asn	Ser	Gln	Met	Ala 345	Gln	Val	Gly	Asp	Gly 350	Asp	Asn	
Ser	Pro	Leu 355		Asn	Asn	Phe	Arg 360	Gln	Tyr	Leu	Pro	Ser 365	Leu	Pro	Gln	
Ser	Val		Cys	Arg	Pro	Phe 375		Phe	Ser	Ala	Gly 380	Lys	Pro	Tyr	Glu	
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Phe	e Lev	ı Lev	ı Tyr	Va]		. Thr	: Phe	e Met	Tyr 410	· Val	. Phe	e Sei	Thr	Phe	e Ala	
Ası	ı Ile	e Lev	1 Arg 420		ı Lys	s Glu	ı Sei	c								
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															gggggca	180

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<212> PRT

<213> Bacteriophage M13mp18

<400> 215

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Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro Ala 20 25 30

Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe Met 35 40 45

Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val Tyr 50 55 60

Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr Gln 65 70 75 80

Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn Gly 85 90 95

Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Pro Phe 100 105 110

Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro Val 115 120 125

Asn Ala Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Glu Gly
130 135 140

Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Ser Glu Gly 145 150 155 160

Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met 165 170 175

Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala 180 185 190

Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr 195 200 205

Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn 210 215 220

Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala 225 230 235 240



Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln 245 250 255

Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe 260 265 270

Ser Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn 275 280 285

Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met 290 295 300

Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser 305 310 315

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<212> DNA

<213> Bacteriophage M13mp18

<400> 216

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<210> 217

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<212> PRT



<213> Bacteriophage M13mp18

<400> 217

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Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly 35 40 45

Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala 50 55 60

Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro 65 70 75 80

Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val 85 90 95

Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser 100 105 110

Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu 115 120 125

Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile 130 135 140

Leu Arg Asn Lys Glu Ser 145 150